by the present amendments.

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Respectfully submitted,

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Marked Up Version of Amendments

In the Specification:

On page 1, line 6, before "This", insert: --This invention was made with Government support under Contract #AI 27849 awarded by the National Institutes of Health. The Government has certain rights in this invention.--

Amend the first full paragraph on page 1 as follows:

This application is a divisional of U.S.S.N. 09/218,950, filed December 22, 1998, now U.S. Patent No. 6,284,240 B1, which is a divisional of U.S.S.N. 08/284,391, filed August 2, 1994, now U.S. Patent No. 5,851,828, which is a continuation-in-part of [Seed et al.,] U.S.S.N. 08/195,395, filed February 14, 1994, now abandoned, which is a continuation-in-part of [Seed et al.,] U.S.S.N. 07/847,566, filed March 6, 1992, now abandoned, which is a continuation-in-part of [Seed et al.,] U.S.S.N. 07/665,961, filed March 7, 1991, now abandoned.

Amend the third full paragraph on page 21 as follows:

FIG. 1A presents the amino acid sequence about the site of fusion between CD4 (residues 1-369) and different receptor chains (SEQ ID NOS: 38-41). The underlined sequence shows the position of the amino acids encoded within the BamHI site used for fusion construction. The beginning of the transmembrane domain is marked

with a vertical bar. The η sequence is identical to the ζ sequence at the amino terminus, but diverges at the carboxyl terminus (Jin et al., Proc. Natl. Acad. Sci. USA 87:3319-3323 (1990)). **FIG. 1B** presents flow cytometric analysis of surface expression of CD4, CD4:ζ, CD4:γ and CD4:η in CV1 cells. Cells were infected with virus expressing CD4 chimeras or $CD16_{PI}$, incubated for 9 hours at 37°C, and stained with phycoerythrin-conjugated anti-CD4 MAb Leu3A.

Amend the first full paragraph on page 24 as follows:

FIG. 7A-B shows characterization of the CD16:ζ chimeric receptor. **FIG. 7A** is a schematic diagram of the CD16:ζ fusion protein. The extracellular portion of the phosphatidylinositol-linked form of monomeric CD16 was joined to dimeric ζ just external to the transmembrane domain. The protein sequence at the fusion junction is shown at the bottom (SEQ ID NOS: 42, 43). **FIG. 7B** shows a flow cytometric analysis of calcium mobilization following crosslinking of the CD16:ζ chimera in either a TCR positive or TCR negative cell line. The mean ratio of violet to blue fluorescence (a measure of relative calcium ion concentration) among cell populations treated with antibodies at time 0 is shown. Solid squares, the response of Jurkat cells to anti-CD3 MAb OKT3; solid triangles, the response of CD16:ζ to anti-CD16 MAb 3G8 crosslinking in the REX33A TCR^- mutant; open squares, the response to CD16:ζ crosslinking in the Jurkat TCR^- mutant line JRT3.T3.5; open triangles, the response to

CD16:ζ crosslinking in Jurkat cells; crosses, the response to nonchimeric CD16 in Jurkat cells; and dots, the response to nonchimeric CD16 in the REX33A TCR^- cell line.

Amend the first full paragraph on page 25 as follows:

FIG. 9A-D shows that elimination of the potential for transmembrane interactions reveals a short ζ segment capable of mediating cytolysis. **FIG. 9A** is a schematic diagram of the monomeric bipartite and tripartite chimeras. At the top is the CD16:ζ construct truncated at residue 65 and lacking transmembrane Cys and Asp residues. Below are the CD16:CD5:ζ and CD16:CD7:ζ constructs and related controls. The peptide sequences of the intracellular domains are shown below (SEQ ID NOS: 45-47). **FIG. 9B** shows the cytolytic activity of monomeric chimera deletion mutants. The cytolytic activity of cells expressing CD16:ζ (solid circles; mfi 495) was compared to that of cells expressing CD16:ζAsp66* (solid squares; mfi 527) or the mutants CD16:ζCys11Gly/Asp15Gly/Asp66*, (open squares; mfi 338) and CD16:ζCys11Gly/Asp15Gly/Glu60* (filled triangles; mfi 259). **FIG. 9C** shows the cytolytic activity mediated by tripartite

Amend the first full paragraph on page 27 as follows:

FIG. 11A-B shows alignment of internal repeats of ζ and comparison of their ability to support cytolysis. **FIG. 11A** is a schematic diagram of chimeras formed

by dividing the ζ intracellular domain into thirds and appending them to the transmembrane domain of a CD16:7 chimera. The sequences of the intracellular domains are shown below (SEQ ID NOS: 48-50), with shared residues boxed, and related residues denoted by asterisks. **FIG. 11B** shows the cytolytic potency of the three ζ subdomains. Solid circles, cells expressing CD16:ζ (mfi 476); solid squares, CD16:7:ζ(33-65) (mfi 68); open squares, CD16:7:ζ(71-104) (mfi 114); and solid triangles, CD16:7:ζ(104-138) (mfi 104).

Amend the first full paragraph on page 28 as follows:

FIG. 15A-E shows identification of residues in the FcRγII A tail (SEQ ID NO: 53) which are important for cytolysis. **FIG. 15A** is a schematic diagram of the deletion constructs. **FIGS. 15B** and **15C** shows calcium mobilization and cytolysis by carboxyl-terminal deletion variants of CD16:FcRγII A. **FIGS. 15D** and **15E** show calcium mobilization and cytolysis by tripartite chimeras bearing progressively less of the amino terminus of the intracellular tail of CD16:FcRγII A.

Amend full paragraphs 1-6 on page 31 as follows:

FIG. 23 shows the nucleic acid (SEQ ID NO: 28) and amino acid (SEQ ID NO: 29) sequence of the D1-D4 domains of CD4 (CD4 Bam).

FIG. 24 shows the nucleic acid (SEQ ID NO: 30) and amino acid (SEQ ID

NO: 31) sequence of the D1-D2 domains of CD4 (CD4 Nhe).

FIG. 25 shows the nucleic acid (SEQ ID NO: 32) and amino acid (SEQ ID NO: 33) sequence of the hinge, CH2, and CH3 domains of human IgG1 (Igh23 Bam).

FIG. 26 shows the nucleic acid (SEQ ID NO: 34) and amino acid (SEQ ID NO: 35) sequence of the transmembrane domain of CD7 (TM7 Bam Mlu).

FIG. 27 shows the nucleic acid (SEQ ID NO: 36) and amino acid (SEQ ID NO: 37) sequence of the intracellular domain of zeta (Zeta Mlu Not).

FIG. 28 shows the DNA sequence (SEQ ID NO: 51) and primary amino acid sequence (SEQ ID NO: 52) of a synthetic alpha helix.

Amend the first full paragraph on page 41 as follows:

To identify the minimal ζ sequences necessary for cytolysis, a series of deletion mutants were prepared in which successively more of the ζ intracellular domain (SEQ ID NO: 44) was removed from the carboxyl terminus (Fig. 8A). Most of the intracellular domain of zeta could be removed with little consequence for cytolytic potential; the full length chimera CD16:ζ was essentially equal in efficacy to the chimera deleted to residue 65, CD16:ζAsp66* (Fig. 8B). A substantial decrease in cytotoxicity was observed on deletion to ζ residue 59 (chimera CD16:ζGlu60*), and further deletion to residue 50 resulted in slightly less activity. However complete loss of activity was not observed even when the intracellular domain was reduced to a three residue

transmembrane anchor (Fig. 8B).

In the Claims:

Add the following new claims 22-30.

--22. An isolated proteinaceous chimeric receptor, said receptor comprising (a) an extracellular portion which includes a CD4 domain that specifically recognizes and binds HIV or an HIV-infected cell but which does not mediate HIV infection, (b) a transmembrane portion, and (c) an intracellular portion which signals a cell bearing said receptor to destroy a receptor-bound HIV or HIV-infected cell.

23. The receptor of claim 22, wherein said CD4 ~~portion~~ domain consists of amino acids 1-394 of SEQ ID NO: 29.

24. The receptor of claim 22, wherein said CD4 portion consists of amino acids 1-200 of SEQ ID NO: 31.

25. The receptor of claim 22, wherein said transmembrane portion comprises the CD7 transmembrane domain of SEQ ID NO: 35.

26. The receptor of claim 22, wherein said extracellular portion further

comprises the IgG1 hinge, CH2, and CH3 domains of SEQ ID NO: 32.

27. The receptor of claim 22, wherein said CD4 portion is projected away from the membrane of a cell bearing said receptor by at least 48 angstroms.

28. The receptor of claim 27, wherein said CD4 portion is projected away from the membrane of a cell bearing said receptor by at least 72 angstroms.

29. The receptor of claim 22, wherein said intracellular portion is the signal-transducing portion of a T cell receptor protein, a B cell receptor protein, or an Fc receptor protein.

30. The receptor of claim 29, wherein said T cell receptor protein is ζ.--